



SEQUENCE LISTING

<110> WANG, HUA
LUO, HONGLIANG
CONNOR, CHRIS
SCHWARTZ, STEVEN
YOUSEF, AHMED
WAN, KAI

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gcgggggaaag gtgcaantgc atcgctgaga gaggagcccg cggcgcatta gctagttggt      240
ggggtaacgg ctcaccaagg cgacgatgcg tagccgacct gagaggggtga ccggccacac      300
tgggactgag acacggccca gactoctacg ggaggcagca gtagggaatc ttccgcaatg      360
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tggtgctcgg	ggagagcggc	aaggggagtg	gaaagcccct	tgngagacgg	taccgagtga	480
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cggaaatcact	gggcgtaaag	cgtgcgtagg	cggttgngta	agtctggagt	gaaagtccan	600
ggctcaaccn	tgggaatgct	ttggaaactg	cntgacttga	gtgctggaga	ggcaagggga	660
attccncgtg	tagcgggtgna	atgcgtagat	atgtggagga	ataccagtgg	cgaangcgcc	720
ttgctggaca	gtgactgacg	ctgaggcacg	aaagcgtggg	gagcaaacag	gattagatac	780
cctggtagtc	cacgccgtaa	acgatgagtg	ctaggtgttg	gggggacaca	ccccagtgcc	840
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aattgacggg	ggcccgacac	agcagtggag	catgtggttt	aattcgaagc	aacgcgaaga	960
accttaccag	ggctngacat	ccctctgaca	gccgcagaga	tgnggnttcc	cttcggggca	1020
gaggagacag	gtggtgcatg	gttgctgtca	gctcgtgtcg	tgagatgttg	ggttaagtcc	1080
cgcaacgagc	gcaacccttg	anctgtgtta	ccagcacggt	gaggtgggga	ctcacagggtg	1140
actgccggcg	taagtccggag	gaaggcgggg	atgacgtcaa	atcatcatgc	cctttatgtc	1200
ctgggctaca	cacgtgctac	aatgggcggg	acaacgggaa	gcgaagccgc	gaggtggagc	1260
aaaacccaaa	aagccgttcg	tagttcggat	tgcaggctgc	aactcgctcg	catgaagccg	1320
gaattgctag	taatcgcgga	tcagcatgcc	gcggtgaatc	cgttcccggg	ccttgtagac	1380
accgcccgtc	acaccacgag	agtcggcaac	accogaagtc	ggtgaggtaa	ccntntnngg	1440
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<210> 79

<211> 718

<212> DNA

<213> Alicyclobacillus acidocaldarius

<400> 79

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tggctgttgg	accggcagat	caccgtgccg	ggcgattggg	tggtgaagcg	cccgaacctc	180
aaccggggcg	gcttcgcgct	ccagttcgac	aacgtgtact	atccggacgt	ggacgacacg	240
gccgtcgta	tctgggcgct	caacacgctg	cgactcccgg	acgagcgccg	caggcgagac	300
gccatgacga	agggattccg	gccatgacga	agggattccg	ctggattgtc	ggcatgcaga	360
gctcgaacgg	cggctggggc	gcatacgacg	tcgacaacac	gagcgatctc	ccgaaccaca	420
tcccgttctg	cgacttcggc	gaagtgaccg	atccgccgtc	ggaagacgtc	accgcccacg	480
tgctcgagtg	tttcggcagc	ttcggctacg	acgacgcctg	gaagggtgatc	cagcgcgcg	540
tggcgtaacct	caagcgggag	cagaagccgg	acggcagctg	gttcgggtcgc	tggggcgta	600
actacgtgta	tggcatcggc	gcggtggtgt	cggcgctgaa	ggcggtcggg	atcgacatgc	660
gcgagccgta	cattcaaaag	gcgctcgatt	gggtggagca	gcatacgaac	ccggacgg	718

<210> 80
 <211> 878
 <212> DNA
 <213> Alicyclobacillus acidocaldarius

<400> 80
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 gcgctgcgcg ctgcggggct tccggccgat cacgaccgct tgggtcaaggc gggcgagtgg 120
 ctggttgacc ggcagatcac ggttccgggc gactgggcgg tgaagcgccc gaacctcaag 180
 ccgggcgggt tcgcgttcca gttcgacaac gtgtactacc cggacgtgga cgacacggcc 240
 gtcgtggtgt gggcgctcaa caccctgcgc ttgccggacg agcgccgcag gcgggacgcc 300
 atgacgaagg gattccgctg gattgtcggc atgcagagct cgaacggcgg ttggggcgcc 360
 tacgacgtcg acaacacgag cgatctcccg aaccacatcc cgttctgcga cttcggcgaa 420
 gtgaccgatc cgccgtcaga ggacgtcacc gccacgtgc tcgagtgttt cggcagcttc 480
 gggtagcatg acgcctggaa ggtcatccgg cgcgcgggtg aatatctcaa gcgggagcag 540
 aagccggacg gcagctgggt cggtcgttgg ggcgtcaatt acctctacgg cacgggcgcg 600
 gtggtgtcgg cgctgaaggc ggtcgggagc gacgcgcgcg agccgtacat tcaaaaggcg 660
 ctcgactggg tcgagcagca tcagaaccgg gacggcggct ggggcgagga ctgccgctcg 720
 tacgaggatc cggcgtacgc gggtaagggc gcgagcaccg cgtcgcagac ggccctggcg 780
 ctgatggcgc tcatcgcggg cggcagggcg gagtccgagg ccgcgcgcgg cgccgtgcaa 840
 tacctcgtgg agacgcagcg cccggacggc ggctggga 878

<210> 81
 <211> 878
 <212> DNA
 <213> Alicyclobacillus acidoterrestris

<400> 81
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 ttggtcagta aacaaattct caaggatggc gactggaaag ttcgtcgacg caaggcgaaa 180
 ccaggcgggt gggcatttga attccactgc gaaaactacc cagacgtcga cgatacggcg 240
 atggtcgtct tggcgctcaa tggcattcaa ttgccggatg aagggaagcg tcgtgacgca 300
 ttgaccggtg gcttccgttg gttgcgcgag atgcagagtt cgaacggggg ctggggcgca 360
 tacgatgtgg acaacacgcg tcagttagacc aatcggattc cattttgcaa cttcggcgaa 420
 gtgattgatc cgccatcgga agacgtcacc gcacacgtct tggagtgtct cggcagcttt 480
 gggtagcagc aggcattggaa ggtgattcgc aaggcggctg agtatctcaa ggcgcaacaa 540
 cgcccagatg ggtcatgggt tggccgctgg ggcgtcaact acgtgtatgg catcggcgcg 600
 gtcgttccgg gactcaaggc cgtcgggtgc gatatgcgtg agccgtgggt gcaaaaagtcg 660
 ctgcactggc tcgtcgagca tcaaaatgag gatggcggct ggggtgaaag ccgaattcca 720
 gcacactggc ggccgttact agtggatccg agctcggtag caagcttggc gtaatcatgg 780
 tcatagctgt ttctgtgtg aaattggat cgcgtcacia ttacacaaac atacgagccg 840
 gaacataagt gtaagcctgg ggtgcctatg agtgagct 878

<210> 82
 <211> 878
 <212> DNA
 <213> Alicyclobacillus acidocaldarius

<400> 82
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 gcactgcgtt cggctggatt gccaccagat catccagcgc tgattaaagc gggtagtggt 120
 ttggtcagta aacaaattct caaggatggc gactggaaag ttcgtcgacg caaggcgaaa 180
 ccaggcgggt gggcatttga attccactgc gaaaactacc cagacgtcga cgatacggcg 240

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atggtcgtct tggcgctcaa tggcattcaa ttgccggatg aagggaaagcg tcgtgacgca 300
ttgacccgtg gcttccgttg gttgcgcgag atgcagagtt cgaacggggg ctggggcgca 360
tacgatgtgg acaacacgcg tcagttgacc aaatcggatt ccatttttgc gacttcgggc 420
gaagtgattg atccgccatc ggaagacgtc accgcacacg tcttggagtg cttcggcagc 480
tttgggtacg acgaggcatg gaaggtgatt cgcaaggcgg tcgagtatct caaggcgcaa 540
caacgcccag atgggtcatg gtttggccgc tggggcgctca actacgtgta tggcatcggc 600
gcggtcgttc cgggactcaa ggccgtcggg gtcgatatgc gtgagccgtg ggtgcaaaag 660
tcgctcgact ggctcgtcga gcatcaaaat gaggatggcg gttgggggtga agattgccgt 720
tcctatgatg atccacgtct cgcaggtcag ggtgtgagta caccgtcgca gaccgcctgg 780
gcgttgatgg cgctcatcgc gggcgggcgt gtcgagtcag atgcgggtatt gcgcggggtc 840
acttaccttc acgacacgca gcgcgcagat ggtggctg 878

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<210> 83

<211> 631

<212> PRT

<213> Alicyclobacillus acidocaldarius

<400> 83

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Met Ala Glu Gln Leu Val Glu Ala Pro Ala Tyr Ala Arg Thr Leu Asp
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Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
      20              25              30

Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
      35              40              45

Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
      50              55              60

Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
      65              70              75              80

Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
      85              90              95

Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
      100              105              110

Ala Leu Arg Phe Ile Gln Ser Gln Gly Gly Ile Glu Ser Ser Arg Val
      115              120              125

Phe Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro Trp Glu Lys
      130              135              140

Val Pro Met Val Pro Pro Glu Ile Met Phe Leu Gly Lys Arg Met Pro
      145              150              155              160

Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr Val Val Ala
      165              170              175

Leu Ser Ile Val Met Ser Arg Gln Pro Val Phe Pro Leu Pro Glu Arg
      180              185              190

Ala Arg Val Pro Glu Leu Tyr Glu Thr Asp Val Pro Pro Arg Arg Arg
      195              200              205

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Gly Ala Lys Gly Gly Gly Gly Trp Ile Phe Asp Ala Leu Asp Arg Ala
 210 215 220
 Leu His Gly Tyr Gln Lys Leu Ser Val His Pro Phe Arg Arg Ala Ala
 225 230 235 240
 Glu Ile Arg Ala Leu Asp Trp Leu Leu Glu Arg Gln Ala Gly Asp Gly
 245 250 255
 Ser Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu
 260 265 270
 Lys Ile Leu Asp Met Thr Gln His Pro Ala Phe Ile Lys Gly Trp Glu
 275 280 285
 Gly Leu Glu Leu Tyr Gly Val Glu Leu Asp Tyr Gly Gly Trp Met Phe
 290 295 300
 Gln Ala Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu Ala
 305 310 315 320
 Leu Arg Ala Ala Gly Leu Pro Ala Asp His Asp Arg Leu Val Lys Ala
 325 330 335
 Gly Glu Trp Leu Leu Asp Arg Gln Ile Thr Val Pro Gly Asp Trp Ala
 340 345 350
 Val Lys Arg Pro Asn Leu Lys Pro Gly Gly Phe Ala Phe Gln Phe Asp
 355 360 365
 Asn Val Tyr Tyr Pro Asp Val Asp Asp Thr Ala Val Val Val Trp Ala
 370 375 380
 Leu Asn Thr Leu Arg Leu Pro Asp Glu Arg Arg Arg Arg Asp Ala Met
 385 390 395 400
 Thr Lys Gly Phe Arg Trp Ile Val Gly Met Gln Ser Ser Asn Gly Gly
 405 410 415
 Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser Asp Leu Pro Asn His Ile
 420 425 430
 Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
 435 440 445
 Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
 450 455 460
 Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
 465 470 475 480
 Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
 485 490 495
 Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
 500 505 510

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
 515 520 525
 Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
 530 535 540
 Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
 545 550 555 560
 Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
 565 570 575
 Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
 580 585 590
 Glu Pro Tyr Tyr Thr Gly Thr Ala Ser Pro Gly Asp Phe Tyr Leu Gly
 595 600 605
 Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
 610 615 620
 Lys Gln Ala Ile Glu Arg Arg
 625 630

<210> 84
 <211> 631
 <212> PRT
 <213> Alicyclobacillus acidocaldarius

<400> 84
 Met Ala Glu Gln Leu Val Glu Ala Pro Ala Tyr Ala Arg Thr Leu Asp
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 Arg Ala Val Glu Tyr Leu Leu Ser Cys Gln Lys Asp Glu Gly Tyr Trp
 20 25 30
 Trp Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu
 35 40 45
 Leu Cys His Ile Leu Asp Arg Val Asp Arg Asp Arg Met Glu Lys Ile
 50 55 60
 Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala Leu
 65 70 75 80
 Tyr Pro Gly Gly Pro Pro Asp Leu Asp Thr Thr Ile Glu Ala Tyr Val
 85 90 95
 Ala Leu Lys Tyr Ile Gly Met Ser Arg Asp Glu Glu Pro Met Gln Lys
 100 105 110
 Ala Leu Arg Phe Ile Gln Ser Gln Gly Gly Ile Glu Ser Ser Arg Val
 115 120 125

Phe	Thr	Arg	Met	Trp	Leu	Ala	Leu	Val	Gly	Glu	Tyr	Pro	Trp	Glu	Lys	130	135	140	
Val	Pro	Met	Val	Pro	Pro	Glu	Ile	Met	Phe	Leu	Gly	Lys	Arg	Met	Pro	145	150	155	160
Leu	Asn	Ile	Tyr	Glu	Phe	Gly	Ser	Trp	Ala	Arg	Ala	Thr	Val	Val	Ala	165	170	175	
Leu	Ser	Ile	Val	Met	Ser	Arg	Gln	Pro	Val	Phe	Pro	Leu	Pro	Glu	Arg	180	185	190	
Ala	Arg	Val	Pro	Glu	Leu	Tyr	Glu	Thr	Asp	Val	Pro	Pro	Arg	Arg	Arg	195	200	205	
Gly	Ala	Lys	Gly	Gly	Gly	Gly	Trp	Ile	Phe	Asp	Ala	Leu	Asp	Arg	Ala	210	215	220	
Leu	His	Gly	Tyr	Gln	Lys	Leu	Ser	Val	His	Pro	Phe	Arg	Arg	Ala	Ala	225	230	235	240
Glu	Ile	Arg	Ala	Leu	Asp	Trp	Leu	Leu	Glu	Arg	Gln	Ala	Gly	Asp	Gly	245	250	255	
Ser	Trp	Gly	Gly	Ile	Gln	Pro	Pro	Trp	Phe	Tyr	Ala	Leu	Ile	Ala	Leu	260	265	270	
Lys	Ile	Leu	Asp	Met	Thr	Gln	His	Pro	Ala	Phe	Ile	Lys	Gly	Trp	Glu	275	280	285	
Gly	Leu	Glu	Leu	Tyr	Gly	Val	Glu	Leu	Asp	Tyr	Gly	Gly	Trp	Met	Phe	290	295	300	
Gln	Ala	Ser	Ile	Ser	Pro	Val	Trp	Asp	Thr	Gly	Leu	Ala	Val	Leu	Ala	305	310	315	320
Leu	Arg	Ala	Ala	Gly	Leu	Pro	Ala	Asp	His	Asp	Arg	Leu	Val	Lys	Ala	325	330	335	
Gly	Glu	Trp	Leu	Leu	Asp	Arg	Gln	Ile	Thr	Val	Pro	Gly	Asp	Trp	Ala	340	345	350	
Val	Lys	Arg	Pro	Asn	Leu	Lys	Pro	Gly	Gly	Phe	Ala	Phe	Gln	Phe	Asp	355	360	365	
Asn	Val	Tyr	Tyr	Pro	Asp	Val	Asp	Asp	Thr	Ala	Val	Val	Val	Trp	Ala	370	375	380	
Leu	Asn	Thr	Leu	Arg	Leu	Pro	Asp	Glu	Arg	Arg	Arg	Arg	Asp	Ala	Met	385	390	395	400
Thr	Lys	Gly	Phe	Arg	Trp	Ile	Val	Gly	Met	Gln	Ser	Ser	Asn	Gly	Gly	405	410	415	
Trp	Gly	Ala	Tyr	Asp	Val	Asp	Asn	Thr	Ser	Asp	Leu	Pro	Asn	His	Ile	420	425	430	

Pro Phe Cys Asp Phe Gly Glu Val Thr Asp Pro Pro Ser Glu Asp Val
 435 440 445
 Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Asp Ala
 450 455 460
 Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Lys
 465 470 475 480
 Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
 485 490 495
 Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Ile Asp Thr Arg
 500 505 510
 Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Val Glu Gln His Gln Asn
 515 520 525
 Pro Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Asp Pro Ala
 530 535 540
 Tyr Ala Gly Lys Gly Ala Ser Thr Pro Ser Gln Thr Ala Trp Ala Leu
 545 550 555 560
 Met Ala Leu Ile Ala Gly Gly Arg Ala Glu Ser Glu Ala Ala Arg Arg
 565 570 575
 Gly Val Gln Tyr Leu Val Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp
 580 585 590
 Glu Pro Tyr Tyr Thr Gly Thr Gly Phe Pro Gly Asp Phe Tyr Leu Gly
 595 600 605
 Tyr Thr Met Tyr Arg His Val Phe Pro Thr Leu Ala Leu Gly Arg Tyr
 610 615 620
 Lys Gln Ala Ile Glu Arg Arg
 625 630

<210> 85

<211> 634

<212> PRT

<213> Alicyclobacillus acidoterrestris

<400> 85

Met Thr Lys Gln Leu Leu Asp Thr Pro Met Val Gln Ala Thr Leu Glu
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 Ala Gly Val Ala His Leu Leu Arg Arg Gln Ala Pro Asp Gly Tyr Trp
 20 25 30
 Trp Ala Pro Leu Leu Ser Asn Val Cys Met Glu Ala Glu Tyr Val Leu
 35 40 45
 Leu Cys His Cys Leu Gly Lys Lys Asn Pro Glu Arg Glu Ala Gln Ile
 50 55 60

Arg	Lys	Tyr	Ile	Ile	Ser	Gln	Arg	Arg	Glu	Asp	Gly	Thr	Trp	Ser	Ile	
65					70					75					80	
Tyr	Pro	Gly	Gly	Pro	Ser	Asp	Leu	Asn	Ala	Thr	Val	Glu	Ala	Tyr	Val	
				85					90					95		
Ala	Leu	Lys	Tyr	Leu	Gly	Glu	Pro	Ala	Ser	Asp	Pro	Gln	Met	Val	Gln	
			100					105					110			
Ala	Lys	Glu	Phe	Ile	Gln	Asn	Glu	Gly	Gly	Ile	Glu	Ser	Thr	Arg	Val	
		115					120					125				
Phe	Thr	Arg	Leu	Trp	Leu	Ala	Met	Val	Gly	Gln	Tyr	Pro	Trp	Asp	Lys	
	130					135					140					
Leu	Pro	Val	Ile	Pro	Pro	Glu	Ile	Met	His	Leu	Pro	Lys	Ser	Val	Pro	
145					150					155					160	
Leu	Asn	Ile	Tyr	Asp	Phe	Ala	Ser	Trp	Ala	Arg	Ala	Thr	Ile	Val	Thr	
				165					170					175		
Leu	Ser	Tyr	Arg	His	Glu	Ser	Pro	Thr	Cys	Asp	Ala	Thr	Ser	Gly	Leu	
		180						185					190			
Cys	Lys	Gly	Ser	Gly	Ile	Val	Arg	Gly	Glu	Gly	Pro	Pro	Lys	Arg	Arg	
		195					200					205				
Ser	Ala	Lys	Gly	Gly	Asp	Ser	Gly	Phe	Phe	Val	Ala	Leu	Asp	Lys	Phe	
	210					215					220					
Leu	Lys	Ala	Tyr	Asn	Lys	Trp	Pro	Ile	Gln	Pro	Gly	Arg	Lys	Ser	Gly	
225					230					235					240	
Glu	Gln	Lys	Ala	Leu	Glu	Trp	Ile	Leu	Ala	His	Gln	Glu	Ala	Asp	Gly	
				245					250					255		
Cys	Trp	Gly	Gly	Ile	Gln	Pro	Pro	Trp	Phe	Tyr	Ala	Leu	Leu	Ala	Leu	
			260					265					270			
Lys	Cys	Leu	Asn	Met	Thr	Asp	His	Pro	Ala	Phe	Val	Lys	Gly	Phe	Glu	
		275					280					285				
Gly	Leu	Glu	Ala	Tyr	Gly	Val	His	Thr	Ser	Asp	Gly	Gly	Trp	Met	Phe	
	290					295					300					
Gln	Ala	Ser	Ile	Ser	Pro	Ile	Trp	Asp	Thr	Gly	Leu	Thr	Val	Leu	Ala	
305					310					315					320	
Leu	Arg	Ser	Ala	Gly	Leu	Pro	Pro	Asp	His	Pro	Ala	Leu	Ile	Lys	Ala	
				325					330					335		
Gly	Glu	Trp	Leu	Val	Ser	Lys	Gln	Ile	Leu	Lys	Asp	Gly	Asp	Trp	Lys	
			340					345					350			
Val	Arg	Arg	Arg	Lys	Ala	Lys	Pro	Gly	Gly	Trp	Ala	Phe	Glu	Phe	His	
			355				360					365				

Cys Glu Asn Tyr Pro Asp Val Asp Asp Thr Ala Met Val Val Leu Ala
 370 375 380
 Leu Asn Gly Ile Gln Leu Pro Asp Glu Gly Lys Arg Arg Asp Ala Leu
 385 390 395 400
 Thr Arg Gly Phe Arg Trp Leu Arg Glu Met Gln Ser Ser Asn Gly Gly
 405 410 415
 Trp Gly Ala Tyr Asp Val Asp Asn Thr Arg Gln Leu Thr Lys Ser Asp
 420 425 430
 Ser Ile Phe Ala Thr Ser Gly Glu Val Ile Asp Pro Pro Ser Glu Asp
 435 440 445
 Val Thr Ala His Val Leu Glu Cys Phe Gly Ser Phe Gly Tyr Asp Glu
 450 455 460
 Ala Trp Lys Val Ile Arg Lys Ala Val Glu Tyr Leu Lys Ala Gln Gln
 465 470 475 480
 Arg Pro Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr
 485 490 495
 Gly Ile Gly Ala Val Val Pro Gly Leu Lys Ala Val Gly Val Asp Met
 500 505 510
 Arg Glu Pro Trp Val Gln Lys Ser Leu Asp Trp Leu Val Glu His Gln
 515 520 525
 Asn Glu Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Asp Asp Pro
 530 535 540
 Arg Leu Ala Gly Gln Gly Val Ser Thr Pro Ser Gln Thr Ala Trp Ala
 545 550 555 560
 Leu Met Ala Leu Ile Ala Gly Gly Arg Val Glu Ser Asp Ala Val Leu
 565 570 575
 Arg Gly Val Thr Tyr Leu His Asp Thr Gln Arg Ala Asp Gly Gly Trp
 580 585 590
 Asp Glu Glu Val Tyr Thr Gly Thr Gly Phe Pro Gly Asp Phe Tyr Leu
 595 600 605
 Ala Tyr Thr Met Tyr Arg Asp Ile Leu Pro Val Trp Ala Leu Gly Arg
 610 615 620
 Tyr Gln Glu Ala Met Gln Arg Ile Arg Gly
 625 630

<210> 86

<211> 556

<212> PRT

<213> Bacillus subtilis

<400> 86
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 Phe Glu Gly Pro Ile Met Thr Asn Ser Phe Phe Ile Leu Leu Thr
 35 40 45
 Ser Leu Asp Glu Gly Glu Asn Glu Lys Glu Leu Ile Ser Ser Leu Ala
 50 55 60
 Ala Gly Ile His Ala Lys Gln Gln Pro Asp Gly Thr Phe Ile Asn Tyr
 65 70 75 80
 Pro Asp Glu Thr Arg Gly Asn Leu Thr Ala Thr Val Gln Gly Tyr Val
 85 90 95
 Gly Met Leu Ala Ser Gly Cys Phe His Arg Thr Glu Pro His Met Lys
 100 105 110
 Lys Ala Glu Gln Phe Ile Ile Ser His Gly Gly Leu Arg His Val His
 115 120 125
 Phe Met Thr Lys Trp Met Leu Ala Ala Asn Gly Leu Tyr Pro Trp Pro
 130 135 140
 Ala Leu Tyr Leu Pro Leu Ser Leu Met Ala Leu Pro Pro Thr Leu Pro
 145 150 155 160
 Ile His Phe Tyr Gln Phe Ser Ser Tyr Ala Arg Ile His Phe Ala Pro
 165 170 175
 Met Ala Val Thr Leu Asn Gln Arg Phe Val Leu Ile Asn Arg Asn Ile
 180 185 190
 Ser Ser Leu His His Leu Asp Pro His Met Thr Lys Asn Pro Phe Thr
 195 200 205
 Trp Leu Arg Ser Asp Ala Phe Glu Glu Arg Asp Leu Thr Ser Ile Leu
 210 215 220
 Leu His Trp Lys Arg Val Phe His Ala Pro Phe Ala Phe Gln Gln Leu
 225 230 235 240
 Gly Leu Gln Thr Ala Lys Thr Tyr Met Leu Asp Arg Ile Glu Lys Asp
 245 250 255
 Gly Thr Leu Tyr Ser Tyr Ala Ser Ala Thr Ile Tyr Met Val Tyr Ser
 260 265 270
 Leu Leu Ser Leu Gly Val Ser Arg Tyr Ser Pro Ile Ile Arg Arg Ala
 275 280 285

Ile Thr Gly Ile Lys Ser Leu Val Thr Lys Cys Asn Gly Ile Pro Tyr
 290 295 300
 Leu Glu Asn Ser Thr Ser Thr Val Trp Asp Thr Ala Leu Ile Ser Tyr
 305 310 315 320
 Ala Leu Gln Lys Asn Gly Val Thr Glu Thr Asp Gly Ser Val Thr Lys
 325 330 335
 Ala Ala Asp Phe Leu Leu Glu Arg Gln His Thr Lys Ile Ala Asp Trp
 340 345 350
 Ser Val Lys Asn Pro Asn Ser Val Pro Gly Gly Trp Gly Phe Ser Asn
 355 360 365
 Ile Asn Thr Asn Asn Pro Asp Cys Asp Asp Thr Thr Ala Val Leu Lys
 370 375 380
 Ala Ile Pro Arg Asn His Ser Pro Ala Ala Trp Glu Arg Gly Val Ser
 385 390 395 400
 Trp Leu Leu Ser Met Gln Asn Asn Asp Gly Gly Phe Ser Ala Phe Glu
 405 410 415
 Lys Asn Val Asn His Pro Leu Ile Arg Leu Leu Pro Leu Glu Ser Ala
 420 425 430
 Glu Asp Ala Ala Val Asp Pro Ser Thr Ala Asp Leu Thr Gly Arg Val
 435 440 445
 Leu His Phe Leu Gly Glu Lys Val Gly Phe Thr Glu Lys His Gln His
 450 455 460
 Ile Gln Arg Ala Val Lys Trp Leu Phe Glu His Gln Glu Gln Asn Gly
 465 470 475 480
 Ser Trp Tyr Gly Arg Trp Gly Val Cys Tyr Ile Tyr Gly Thr Trp Ala
 485 490 495
 Ala Leu Thr Gly Met His Ala Cys Gly Leu Thr Glu Ser Ile Pro Val
 500 505 510
 Tyr Lys Arg Leu Cys Val Gly Ser Asn Pro Tyr Lys Met Met Thr Glu
 515 520 525
 Ala Gly Glu Asn Pro Ala Lys Ala Pro Lys Ser Lys His Met Tyr Arg
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 Phe Ile Glu Glu Pro Leu Tyr Lys Arg Pro Gly Leu
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<210> 87

<211> 706

<212> PRT

<213> Dictyostelium discoideum

<400> 87

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Arg Gln Thr Trp Glu Tyr Ser Gln Glu Lys Lys Glu Ala Thr Asp Val
          20           25           30

Asp Ile His Leu Leu Arg Leu Lys Glu Pro Gly Thr His Cys Pro Glu
          35           40           45

Gly Cys Asp Leu Asn Arg Ala Lys Thr Pro Gln Gln Ala Ile Lys Lys
          50           55           60

Ala Phe Gln Tyr Phe Ser Lys Val Gln Thr Glu Asp Gly His Trp Ala
          65           70           75           80

Gly Asp Tyr Gly Gly Pro Met Phe Leu Leu Pro Gly Leu Val Ile Thr
          85           90           95

Cys Tyr Val Thr Gly Tyr Gln Leu Pro Glu Ser Thr Gln Arg Glu Ile
          100          105          110

Ile Arg Tyr Leu Phe Asn Arg Gln Asn Pro Val Asp Gly Gly Trp Gly
          115          120          125

Leu His Ile Glu Ala His Ser Asp Ile Phe Gly Thr Thr Leu Gln Tyr
          130          135          140

Val Ser Leu Arg Leu Leu Gly Val Pro Ala Asp His Pro Ser Val Val
          145          150          155          160

Lys Ala Arg Thr Phe Leu Leu Gln Asn Gly Gly Ala Thr Gly Ile Pro
          165          170          175

Ser Trp Gly Lys Phe Trp Leu Ala Thr Leu Asn Ala Tyr Asp Trp Asn
          180          185          190

Gly Leu Asn Pro Ile Pro Ile Glu Phe Trp Leu Leu Pro Tyr Asn Leu
          195          200          205

Pro Ile Ala Pro Gly Arg Trp Trp Cys His Cys Arg Met Val Tyr Leu
          210          215          220

Pro Met Ser Tyr Ile Tyr Ala Lys Lys Thr Thr Gly Pro Leu Thr Asp
          225          230          235          240

Leu Val Lys Asp Leu Arg Arg Glu Ile Tyr Cys Gln Glu Tyr Glu Lys
          245          250          255

Ile Asn Trp Ser Glu Gln Arg Asn Asn Ile Ser Lys Leu Asp Met Tyr
          260          265          270

Tyr Glu His Thr Ser Leu Leu Asn Val Ile Asn Gly Ser Leu Asn Ala
          275          280          285

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Tyr Glu Lys Val His Ser Lys Trp Leu Arg Asp Lys Ala Ile Asp Tyr
 290 295 300
 Thr Phe Asp His Ile Arg Tyr Glu Asp Glu Gln Thr Lys Tyr Ile Asp
 305 310 315 320
 Ile Gly Pro Val Asn Lys Thr Val Asn Met Leu Cys Val Trp Asp Arg
 325 330 335
 Glu Gly Lys Ser Pro Ala Phe Tyr Lys His Ala Asp Arg Leu Lys Asp
 340 345 350
 Tyr Leu Trp Leu Ser Phe Asp Gly Met Lys Met Gln Gly Tyr Asn Gly
 355 360 365
 Ser Gln Leu Trp Asp Thr Ala Phe Thr Ile Gln Ala Phe Met Glu Ser
 370 375 380
 Gly Ile Ala Asn Gln Phe Gln Asp Cys Met Lys Leu Ala Gly His Tyr
 385 390 395 400
 Leu Asp Ile Ser Gln Val Pro Glu Asp Ala Arg Asp Met Lys His Tyr
 405 410 415
 His Arg His Tyr Ser Lys Gly Ala Trp Pro Phe Ser Thr Val Asp His
 420 425 430
 Gly Trp Pro Ile Ser Asp Cys Thr Ala Glu Gly Ile Lys Ser Ala Leu
 435 440 445
 Ala Leu Arg Ser Leu Pro Phe Ile Glu Pro Ile Ser Leu Asp Arg Ile
 450 455 460
 Ala Asp Gly Ile Asn Val Leu Leu Thr Leu Gln Asn Gly Asp Gly Gly
 465 470 475 480
 Trp Ala Ser Tyr Glu Asn Thr Arg Gly Pro Lys Trp Leu Glu Lys Phe
 485 490 495
 Asn Pro Ser Glu Val Phe Gln Asn Ile Met Ile Asp Tyr Ser Tyr Val
 500 505 510
 Glu Cys Ser Ala Ala Cys Ile Gln Ala Met Ser Ala Phe Arg Lys His
 515 520 525
 Ala Pro Asn His Pro Arg Ile Lys Glu Ile Asn Arg Ser Ile Ala Arg
 530 535 540
 Gly Val Lys Phe Ile Lys Ser Ile Gln Arg Gln Asp Gly Ser Trp Leu
 545 550 555 560
 Gly Ser Trp Gly Ile Cys Phe Thr Tyr Gly Thr Trp Phe Gly Ile Glu
 565 570 575
 Gly Leu Val Ala Ser Gly Glu Pro Leu Thr Ser Pro Ser Ile Val Lys
 580 585 590

Ala Cys Lys Phe Leu Ala Ser Lys Gln Arg Ala Asp Gly Gly Trp Gly
595 600 605

Glu Ser Phe Lys Ser Asn Val Thr Lys Glu Tyr Val Gln His Glu Thr
610 615 620

Ser Gln Val Val Asn Thr Gly Trp Ala Leu Leu Ser Leu Met Ser Ala
625 630 635 640

Lys Tyr Pro Asp Arg Glu Cys Ile Glu Arg Gly Ile Lys Phe Leu Ile
645 650 655

Gln Arg Gln Tyr Pro Asn Gly Asp Phe Pro Gln Glu Ser Ile Ile Gly
660 665 670

Val Phe Asn Phe Asn Cys Met Ile Ser Tyr Ser Asn Tyr Lys Asn Ile
675 680 685

Phe Pro Leu Trp Ala Leu Ser Arg Tyr Asn Gln Leu Tyr Leu Lys Ser
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Lys Ile
705

<210> 88
<211> 647
<212> PRT
<213> Synechocystis PCC6803

<400> 88
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Tyr Ala Asp Gly Tyr Trp Trp Ser Glu Leu Glu Ser Asn Val Thr Ile
35 40 45

Thr Ala Glu Val Val Ile Leu His Lys Ile Trp Gly Thr Ala Ala Gln
50 55 60

Arg Pro Leu Glu Lys Ala Lys Asn Tyr Leu Leu Gln Gln Gln Arg Asp
65 70 75 80

His Gly Gly Trp Glu Leu Tyr Tyr Gly Asp Gly Gly Glu Leu Ser Thr
85 90 95

Ser Val Glu Ala Tyr Thr Ala Leu Arg Ile Leu Gly Val Pro Ala Thr
100 105 110

Asp Pro Ala Leu Val Lys Ala Lys Asn Phe Ile Val Gly Arg Gly Gly
115 120 125

Ile	Ser	Lys	Ser	Arg	Ile	Phe	Thr	Lys	Met	His	Leu	Ala	Leu	Ile	Gly	130	135	140
Cys	Tyr	Asp	Trp	Arg	Gly	Thr	Pro	Ser	Ile	Pro	Pro	Trp	Val	Met	Leu	145	150	155
Leu	Pro	Asn	Asn	Phe	Phe	Phe	Asn	Ile	Tyr	Glu	Met	Ser	Ser	Trp	Ala	165	170	175
Arg	Ser	Ser	Thr	Val	Pro	Leu	Met	Ile	Val	Cys	Asp	Gln	Lys	Pro	Val	180	185	190
Tyr	Asp	Ile	Ala	Gln	Gly	Leu	Arg	Val	Asp	Glu	Leu	Tyr	Ala	Glu	Gly	195	200	205
Met	Glu	Asn	Val	Gln	Tyr	Lys	Leu	Pro	Glu	Ser	Gly	Thr	Ile	Trp	Asp	210	215	220
Ile	Phe	Ile	Gly	Leu	Asp	Ser	Leu	Phe	Lys	Leu	Gln	Glu	Gln	Ala	Lys	225	230	235
Val	Val	Pro	Phe	Arg	Glu	Gln	Gly	Leu	Ala	Leu	Ala	Glu	Lys	Trp	Ile	245	250	255
Leu	Glu	Arg	Gln	Glu	Val	Ser	Gly	Asp	Trp	Gly	Gly	Ile	Ile	Pro	Ala	260	265	270
Met	Leu	Asn	Ser	Leu	Leu	Ala	Leu	Lys	Val	Leu	Gly	Tyr	Asp	Val	Asn	275	280	285
Asp	Leu	Tyr	Val	Gln	Arg	Gly	Leu	Ala	Ala	Ile	Asp	Asn	Phe	Ala	Val	290	295	300
Glu	Thr	Glu	Asp	Ser	Tyr	Ala	Ile	Gln	Ala	Cys	Val	Ser	Pro	Val	Trp	305	310	315
Asp	Thr	Ala	Trp	Val	Val	Arg	Ala	Leu	Ala	Glu	Ala	Asp	Leu	Gly	Lys	325	330	335
Asp	His	Pro	Ala	Leu	Val	Lys	Ala	Gly	Gln	Trp	Leu	Leu	Asp	Lys	Gln	340	345	350
Ile	Leu	Thr	Tyr	Gly	Asp	Trp	Gln	Ile	Lys	Asn	Pro	His	Gly	Glu	Pro	355	360	365
Gly	Ala	Trp	Ala	Phe	Glu	Phe	Asp	Asn	Asn	Phe	Tyr	Pro	Asp	Ile	Asp	370	375	380
Asp	Thr	Cys	Val	Val	Met	Met	Ala	Leu	Gln	Gly	Ile	Thr	Leu	Pro	Asp	385	390	395
Glu	Glu	Arg	Lys	Gln	Gly	Ala	Ile	Asn	Lys	Ala	Leu	Gln	Trp	Ile	Ala	405	410	415
Thr	Met	Gln	Cys	Lys	Thr	Gly	Gly	Trp	Ala	Ala	Phe	Asp	Ile	Asp	Asn	420	425	430

Asp Gln Asp Trp Leu Asn Gln Leu Pro Tyr Gly Asp Leu Lys Ala Met
 435 440 445
 Ile Asp Pro Ser Thr Ala Asp Ile Thr Ala Arg Val Val Glu Met Leu
 450 455 460
 Gly Ala Cys Gly Leu Thr Met Asp Ser Pro Arg Val Glu Arg Gly Leu
 465 470 475 480
 Thr Tyr Leu Leu Gln Glu Gln Glu Gln Asp Gly Ser Trp Phe Gly Arg
 485 490 495
 Trp Gly Val Asn Tyr Leu Tyr Gly Thr Ser Gly Ala Leu Ser Ala Leu
 500 505 510
 Ala Ile Tyr Asp Ala Gln Arg Phe Ala Pro Gln Ile Lys Thr Ala Ile
 515 520 525
 Ala Trp Leu Leu Ser Cys Gln Asn Ala Asp Gly Gly Trp Gly Glu Thr
 530 535 540
 Cys Glu Ser Tyr Lys Asn Lys Gln Leu Lys Gly Gln Gly Asn Ser Thr
 545 550 555 560
 Ala Ser Gln Thr Ala Trp Ala Leu Ile Gly Leu Leu Asp Ala Leu Lys
 565 570 575
 Tyr Leu Pro Ser Leu Gly Gln Asp Ala Lys Leu Thr Thr Ala Ile Glu
 580 585 590
 Gly Gly Val Ala Phe Leu Val Gln Gly Gln Thr Pro Lys Gly Thr Trp
 595 600 605
 Glu Glu Ala Glu Tyr Thr Gly Thr Gly Phe Pro Cys His Phe Tyr Ile
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 Arg Tyr His Tyr Tyr Arg Gln Tyr Phe Pro Leu Ile Ala Leu Ala Arg
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 Tyr Ser His Leu Gln Ala Ser
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<210> 89
 <211> 680
 <212> PRT
 <213> Streptomyces coelicolor

<400> 89
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 Gly Val Pro Glu Ala Ala Ala Arg Ala Thr Arg Arg Ala Thr Asp Phe
 35 40 45

Leu Leu Ala Lys Gln Asp Ala Glu Gly Trp Trp Lys Gly Asp Leu Glu
 50 55 60
 Thr Asn Val Thr Met Asp Ala Glu Asp Leu Leu Leu Arg Gln Phe Leu
 65 70 75 80
 Gly Ile Gln Asp Glu Glu Thr Thr Arg Ala Ala Ala Leu Phe Ile Arg
 85 90 95
 Gly Glu Gln Arg Glu Asp Gly Thr Trp Ala Thr Phe Tyr Gly Gly Pro
 100 105 110
 Gly Glu Leu Ser Thr Thr Ile Glu Ala Tyr Val Ala Leu Arg Leu Ala
 115 120 125
 Gly Asp Ser Pro Glu Ala Pro His Met Ala Arg Ala Ala Glu Trp Ile
 130 135 140
 Arg Ser Arg Gly Gly Ile Ala Ser Ala Arg Val Phe Thr Arg Ile Trp
 145 150 155 160
 Leu Ala Leu Phe Gly Trp Trp Lys Trp Asp Asp Leu Pro Glu Leu Pro
 165 170 175
 Pro Glu Leu Ile Tyr Phe Pro Thr Trp Val Pro Leu Asn Ile Tyr Asp
 180 185 190
 Phe Gly Cys Trp Ala Arg Gln Thr Ile Val Pro Leu Thr Ile Val Ser
 195 200 205
 Ala Lys Arg Pro Val Arg Pro Ala Pro Phe Pro Leu Asp Glu Leu His
 210 215 220
 Thr Asp Pro Ala Arg Pro Asn Pro Pro Arg Pro Leu Ala Pro Val Ala
 225 230 235 240
 Ser Trp Asp Gly Ala Phe Gln Arg Ile Asp Lys Ala Leu His Ala Tyr
 245 250 255
 Arg Lys Val Ala Pro Arg Arg Leu Arg Arg Ala Ala Met Asn Ser Ala
 260 265 270
 Ala Arg Trp Ile Ile Glu Arg Gln Glu Asn Asp Gly Cys Trp Gly Gly
 275 280 285
 Ile Gln Pro Pro Ala Val Tyr Ser Val Ile Ala Leu Tyr Leu Leu Gly
 290 295 300
 Tyr Asp Leu Glu His Pro Val Met Arg Ala Gly Leu Glu Ser Leu Asp
 305 310 315 320
 Arg Phe Ala Val Trp Arg Glu Asp Gly Ala Arg Met Ile Glu Ala Cys
 325 330 335
 Gln Ser Pro Val Trp Asp Thr Cys Leu Ala Thr Ile Ala Leu Ala Asp
 340 345 350

Ala Gly Val Pro Glu Asp His Pro Gln Leu Val Lys Ala Ser Asp Trp
 355 360 365
 Met Leu Gly Glu Gln Ile Val Arg Pro Gly Asp Trp Ser Val Lys Arg
 370 375 380
 Pro Gly Leu Pro Pro Gly Gly Trp Ala Phe Glu Phe His Asn Asp Asn
 385 390 395 400
 Tyr Pro Asp Ile Asp Asp Thr Ala Glu Val Val Leu Ala Leu Arg Arg
 405 410 415
 Val Arg His His Asp Pro Glu Arg Val Glu Lys Ala Ile Gly Arg Gly
 420 425 430
 Val Arg Trp Asn Leu Gly Met Gln Ser Lys Asn Gly Ala Trp Gly Ala
 435 440 445
 Phe Asp Val Asp Asn Thr Ser Ala Phe Pro Asn Arg Leu Pro Phe Cys
 450 455 460
 Asp Phe Gly Glu Val Ile Asp Pro Pro Ser Ala Asp Val Thr Ala His
 465 470 475 480
 Val Val Glu Met Leu Ala Val Glu Gly Leu Ala His Asp Pro Arg Thr
 485 490 495
 Arg Arg Gly Ile Gln Trp Leu Leu Asp Ala Gln Glu Thr Asp Gly Ser
 500 505 510
 Trp Phe Gly Arg Trp Gly Val Asn Tyr Val Tyr Gly Thr Gly Ser Val
 515 520 525
 Ile Pro Ala Leu Thr Ala Ala Gly Leu Pro Thr Ser His Pro Ala Ile
 530 535 540
 Arg Arg Ala Val Arg Trp Leu Glu Ser Val Gln Asn Glu Asp Gly Gly
 545 550 555 560
 Trp Gly Glu Asp Leu Arg Ser Tyr Arg Tyr Val Arg Glu Trp Ser Gly
 565 570 575
 Arg Gly Ala Ser Thr Ala Ser Gln Thr Gly Trp Ala Leu Met Ala Leu
 580 585 590
 Leu Ala Ala Gly Glu Arg Asp Ser Lys Ala Val Glu Arg Gly Val Ala
 595 600 605
 Trp Leu Ala Ala Thr Gln Arg Glu Asp Gly Ser Trp Asp Glu Pro Tyr
 610 615 620
 Phe Thr Gly Thr Gly Phe Pro Trp Asp Phe Ser Ile Asn Tyr Asn Leu
 625 630 635 640
 Tyr Arg Gln Val Phe Pro Leu Thr Ala Leu Gly Arg Tyr Val His Gly
 645 650 655

Glu Pro Phe Ala Lys Lys Pro Arg Ala Ala Asp Ala Pro Ala Glu Ala
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Ala Pro Ala Glu Val Lys Gly Ser
 675 680

<210> 90

<211> 741

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Figure 6
 majority sequence

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<223> Variable amino acid or not present

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<222> (238)..(241)

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<221> MOD_RES

<222> (263)..(263)

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<222> (293)..(294)
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<222> (504)..(504)
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<222> (622)..(622)
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 <223> Variable amino acid or not present

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 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Ala Val Ala Arg Ala Leu Asp Arg
 50 55 60

Ala Val Asp Tyr Leu Leu Ser Arg Gln Lys Ala Asp Gly Tyr Trp Trp
 65 70 75 80

Gly Pro Leu Leu Ser Asn Val Thr Met Glu Ala Glu Tyr Val Leu Leu
 85 90 95

Cys His Ile Leu Gly Arg Val Asp Arg Glu Arg Xaa Xaa Met Glu Lys
 100 105 110

Ile Arg Arg Tyr Leu Leu His Glu Gln Arg Glu Asp Gly Thr Trp Ala
 115 120 125

Leu Tyr Pro Gly Gly Pro Xaa Gly Asp Leu Ser Thr Thr Val Glu Ala
 130 135 140

Tyr Val Ala Leu Lys Tyr Leu Gly Xaa Val Ser Ala Asp Glu Pro His
 145 150 155 160

Met Val Lys Ala Leu Glu Phe Ile Gln Ser Gln Gly Gly Ile Glu Ser
 165 170 175

Ser Arg Val Phe Thr Arg Met Trp Leu Ala Leu Val Gly Glu Tyr Pro
 180 185 190

Trp Asp Lys Leu Pro Met Ile Pro Pro Glu Ile Met Leu Leu Pro Lys
 195 200 205

Asn Val Pro Leu Asn Ile Tyr Glu Phe Gly Ser Trp Ala Arg Ala Thr
 210 215 220

Val Val Pro Leu Ser Ile Val Met Ala Gln Gln Pro Val Xaa Xaa Xaa
 225 230 235 240

Xaa Phe Pro Leu Pro Glu Leu Ala Arg Val Pro Glu Leu Tyr Glu Thr
 245 250 255

Asp Val Pro Pro Arg Arg Xaa Arg Gly Ala Lys Gly Gly Gly Gly Trp
 260 265 270

Xaa Xaa Xaa Ile Phe Asp Ala Xaa Xaa Leu Asp Ser Ala Leu His Gly
 275 280 285

Tyr Gln Lys Ala Xaa Xaa Ala Val His Pro Phe Arg Arg Ala Gly Glu
 290 295 300

Ala Arg Ala Leu Thr Trp Ile Leu Glu Arg Gln Glu Gly Asp Gly Ser
 305 310 315 320

Trp Gly Gly Ile Gln Pro Pro Trp Phe Tyr Ala Leu Ile Ala Leu Lys
 325 330 335

Val Leu Gly Met Thr Xaa Gln His Pro Ala Phe Ile Lys Gly Leu Glu
 340 345 350

Gly Leu Glu Leu Tyr Gly Val Glu Leu Ser Asp Gly Gly Trp Met Phe
 355 360 365

Gln Ala Xaa Ser Ile Ser Pro Val Trp Asp Thr Gly Leu Ala Val Leu
 370 375 380

Ala Leu Arg Ala Ala Gly Leu Pro Ala Asp His Pro Ala Leu Val Lys
 385 390 395 400

Ala Gly Glu Trp Leu Leu Asp Arg Gln Ile Thr Val Pro Gly Asp Trp
 405 410 415

Ala Val Lys Arg Xaa Xaa Pro Asn Leu Lys Pro Gly Gly Trp Ala Phe
 420 425 430

Glu Phe Asp Asn Val Asn Tyr Pro Asp Val Asp Asp Thr Ala Val Val
 435 440 445

Val Xaa Xaa Xaa Leu Ala Leu Asn Gly Leu Arg Leu Pro Asp Glu Glu
 450 455 460

Arg Arg Arg Asp Ala Ile Thr Lys Gly Phe Arg Trp Leu Leu Gly Met
 465 470 475 480

Gln Ser Ser Asn Gly Gly Trp Gly Ala Tyr Asp Val Asp Asn Thr Ser
 485 490 495

Asp Leu Pro Asn His Leu Pro Xaa Phe Cys Asp Phe Gly Glu Val Xaa
 500 505 510

Ile Asp Pro Pro Ser Ala Asp Val Thr Ala His Val Leu Glu Cys Leu
 515 520 525

Gly Ser Xaa Xaa Xaa Phe Gly Xaa Xaa Xaa Xaa Xaa Tyr Asp Glu Ala
 530 535 540

Trp Lys Val Ile Arg Arg Ala Val Glu Tyr Leu Lys Arg Glu Gln Glu
 545 550 555 560

Gln Asp Gly Ser Trp Phe Gly Arg Trp Gly Val Asn Tyr Leu Tyr Gly
 565 570 575

Thr Gly Ala Val Val Ser Ala Leu Lys Ala Val Gly Leu Asp Thr Arg
 580 585 590

Glu Pro Tyr Ile Gln Lys Ala Leu Asp Trp Leu Glu Ser His Gln Asn
 595 600 605

Ala Asp Gly Gly Trp Gly Glu Asp Cys Arg Ser Tyr Glu Xaa Asp Pro
 610 615 620

Glu Tyr Ala Gly Gln Gly Ala Ser Thr Ala Ser Gln Thr Ala Trp Ala
 625 630 635 640

Leu Met Ala Leu Ile Ala Gly Xaa Xaa Xaa Xaa Xaa Xaa Gly Arg
 645 650 655

Ala Glu Xaa Xaa Ser Glu Ala Ala Glu Arg Gly Val Ala Tyr Leu Val
 660 665 670

Glu Thr Gln Arg Pro Asp Gly Gly Trp Asp Glu Pro Tyr Tyr Thr Gly
 675 680 685

Thr Gly Phe Pro Gly Asp Phe Tyr Leu Gly Tyr Thr Met Tyr Arg Gln
 690 695 700

Val Phe Pro Leu Leu Ala Leu Gly Arg Tyr Lys Gln Ala Xaa Xaa Xaa
 705 710 715 720

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 725 730 735

Glu Arg Xaa Gly Ser
 740

<210> 91
 <211> 376
 <212> DNA
 <213> *Zygosaccharomyces bailii*

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 tatcggtttc aagccgatgg aagtttgagg caataacagg tctgtgatgc ccttagacgt 180
 tctggggccgc acgcgcgcta cactgacgga gccagcgagt ctaaccttgg ccgagagggtc 240
 tgggtaatct tgtgaaactc cgctcgtgctg gggatagagc attgtaatta ttgctcttca 300
 acgaggaatt cctagtaagc gcaagtcac aacttgcgtt gattacgtcc ctgccctttg 360

tacacacaag ccgaat

376

<210> 92

<211> 404

<212> DNA

<213> *Saccharomyces humaticus*

<400> 92

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tggttatcca cttcttagag ggactatcgg tttcaagccg atggaagttt gaggcaataa 180
caggtctgtg atgcccttag acgttctggg ccgcacgcgc gctacactga cggagccagc 240
gagtctaacc ttggccgaga ggtcttggtg atcttgtgaa actccgtcgt gctggggata 300
gagcattgta attattgctc ttcaacgagg aattcctagt aagcgcaagt catcagcttg 360
cgttgattac gtccctgccc tttgtacaca ccgccgctcg ctag 404
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<210> 93

<211> 408

<212> DNA

<213> *Candida colliculosa*

<400> 93

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tggttatcca cttcttagag ggactatcgg tttcaagccg atggaagttt gaggcaataa 180
caggtctgtg atgcccttag acgttctggg ccgcacgcgc gctacactga cggagccagc 240
gagtctaacc ttggccgaga ggtctgggta atcttgtgaa actccgtcgt gctggggata 300
gagcattgta attattgctc ttcaacgagg aattcctagt aagcgcaagt catcagcttg 360
cgttgattac gtccctgccc tttgtacaca ccgccgctcg ctagtacc 408
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<210> 94

<211> 303

<212> DNA

<213> *Vitis vinifera*

<400> 94

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ctccgcagcc agcttcttag agggactatg gccgcttagg ccaaggaagt ttgaggcaat 180
aacagggtctg tgatgccctt agatgttctg ggccgcacgc gcgctacact gatgtattca 240
acgagtctat agccttggcc gacaggcccc ggtaatcttt gaaatttcat cgtgatgggg 300
ata 303
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<210> 95

<211> 407

<212> DNA

<213> *Zygosaccharomyces rouxii*

<400> 95

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tggtttttcc acttcttaga gggactatcg gtttcaagcc gatggaagtt tgaggcaata 180
acagggtctg gatgccctta gacgttctgg gccgcacgcg cgctacactg acggagccaa 240
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cgagtctaac cttggccgag aggtctgggt aatcttgtga aactccgtcg tgctggggat 300
 agagcattgt aattattgct cttcaacgag gaattcctag taagcgcaag tcatcagctt 360
 gcgttgatta cgtccctgcc ctttgtacac accgcccgtc gctagta 407

<210> 96

<211> 393

<212> DNA

<213> *Penicillium digitatum*

<400> 96

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 tgcgataacg aacgagacct cggcccttaa atagcccgtt ccgcatttgc gggccgctgg 120
 cttcttaagg ggactatcgg ctcaagccga tggaagtgcg cggcaataac aggtctgtga 180
 tgcccttaga tgttctgggc cgcacgcgcg ctacactgac agggccagcg agtacatcac 240
 cttaacgag aggtttgggt aatcttggtt aaccctgtcg tgctggggat agagcattgc 300
 aattattgct cttcaacgag gaatgcctag taggcacgag tcatcagctc gtgccgatta 360
 cgtccctgcc ctttgtacac acaagccgaa ttc 393

<210> 97

<211> 400

<212> DNA

<213> *Byssoschlamys fulva*

<400> 97

tgctggaatt cggctttgca tggccgttct tagttggtgg agtgatttgt ctgcttaatt 60
 gcgataacga acgagacctc ggctcttaaa tagcccgttc cgcgtttgcg ggccgctggc 120
 ttcttagggg gactatcggc tcaagccgat ggaagtgcgc ggcaataaca ggtctgtaat 180
 gcccttagat gttctggggc gcacgcgcgc tacactgaca gggccagcgg gtacatcacc 240
 ttggccgaga ggtctgggta atcttggttaa accctgtcgt gctggggata gagcattgca 300
 attattgctc ttcaacgagg aatgcctagt aggcacgagt catcagctcg tgccgattac 360
 gtccctgccc tttgtacaca caagccgaat tctgcagata 400

<210> 98

<211> 416

<212> DNA

<213> *Penicillium chrysogenum*

<400> 98

tctttcttga tcttttggat ggtggtgcat ggccgttctt agttggtgga gtgatttgtc 60
 tgcttaattg cgataacgaa cgagacctcg gcccttaaat agcccgttcc gcatttgcgg 120
 gccgctggct tcttaggggg actatcggct caagccgatg gaagtgcgcg gcaataacag 180
 gtctgtgatg cccttagatg ttctggggccg cgcgcgcgt acactgacag ggccagcgag 240
 tacatcacct taaccgagag gtttgggtaa tcttggttaa ccctgtcgtg ctggggatag 300
 agcattgcaa ttattgctct tcaacgagga atgcctagta ggcacgagtc atcagctcgt 360
 gccgattacg tccctgcctt ttgtacacac cgcccgtcgc tactaccgat tgaatg 416

<210> 99

<211> 406

<212> DNA

<213> *Aspergillus nidulans*

<400> 99

agctctttct tgatcttttg gatggtggtg catggccgtt cttagttggt ggagtgattt 60

```

gtctgcttaa ttgcgataac gaacgagacc tcggccctta aatagcccgg tccgcgtccg 120
cgggccgctg gcttcttagg gggactatcg gctcaagccg atggaagtgc gcggaataaa 180
caggtctgtg atgcccttag atgttctggg ccgcacgcgc gctacactga cagggccagc 240
gagtacatca ccttggccga gagggccggg taatcttgtt aaaccctgtc gtgctgggga 300
tagagcattg caattattgc tcttcaacga ggaatgccta gtaggcacga gtcatacagc 360
cgtgccgatt acgtccctgc cctttgtaca caccgcccgt cgctac 406

```

<210> 100

<211> 427

<212> DNA

<213> Eurotium amstelodami

<400> 100

```

tttcttgatc ttttggatgg tgggtgcatgg ccgttcttag ttggtggagt gatttgtctg 60
cttaattgcg ataacgaacg agacctcggc ccttaaataag cccgggtccgc atttgccggc 120
cgctggcttc ttagggggac tatcgggtca agccgatgga agtgccggcg aataacaggt 180
ctgtgatgcc cttagatggt ctgggcccga cgcgcgctac actgacaggg ccagcgagta 240
catcacctta accgagaggt ctgggtaatc ttgttaaacc ctgtcgtgct ggggatagag 300
cattgcaatt attgctcttc aacgaggaat gcctagtagg cacgagtcac cagctcgtgc 360
cgattacgtc cctgcccttt gtacacaccg cccgtcgcta ctaccgattg aatggctcgg 420
tgaggcc 427

```

<210> 101

<211> 442

<212> DNA

<213> Aspergillus candidus

<400> 101

```

ctctttcttg atcttttggg tgggtggtgca tggccgttct tagttggtgg agtgatttgt 60
ctgcttaatt gcgataacga acgagacctc ggcccttaaa tagcccggtc cgcatttgcg 120
ggccgctggc ttcttagggg gactatcggc tcaagccgat ggaagtgcgc ggcaataaca 180
ggtctgtgat gcccttagat gttctggggc gcacgcgcgc tacactgaca gggccagcga 240
gtacatcacc ttggccgaga ggtctgggta atcttggttaa accctgtcgt gctggggata 300
gagcattgca attattgctc ttcaacgagg aatgcctagt aggcacgagt catcagctcg 360
tgccgattac gtccctgccc tttgtacaca ccgcccgctc ctactaccga ttgaatggct 420
cgggtgaggcc tccggactgg ct 442

```

<210> 102

<211> 407

<212> DNA

<213> Gallus gallus

<400> 102

```

ctctttctcg attccgtggg tgggtggtgca tggccgttct tagttggtgg agcgatttgt 60
ctgggtaatt ccgataacga acgagactct ggcatgctaa ctagttagcg gacccccgag 120
cggtcggcgt ccaacttctt agagggacaa gtggcgttca gccacccgag attgagcaat 180
aacaggctctg tgatgccctt agatgtccgg ggctgcacgc gcgctacact gactggctca 240
gcttggtgtct accctacgcc ggcaggcgcg ggtaaccctg tgaaccccat tcgtgatggg 300
gatcggggat tgcaattatt ccccatgaac gaggaattcc cagtaagtgc gggtcataag 360
ctcgcgttga ttaagtccct gccctttgta cacaccgcc gtcgcta 407

```

<210> 103

<211> 407

<212> DNA

<213> *Triticum aestivum*

<400> 103

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ctctttcttg attctatggg tgggtggtgca tggccgttct tagttggtgg agcgatttgt 60
ctggttaatt ccgttaacga acgagacctc agcctgctaa ctagctatgc ggagccatcc 120
ctccgcagct agcttcttag agggactatc gccgtttagg cgacggaagt ttgaggcaat 180
aacaggtctg tgatgccctt agatgttctg ggccgcacgc gcgctacact gatgtattca 240
acgagtatat agccttggcc gacaggcccg ggtaatcttg ggaaatttca tcgtgatggg 300
gatagatcat tgcaattggt ggtcttcaac gaggaatgcc tagtaagcgc gagtcatcag 360
ctcgcgttga ctacgtccct gccctttgta cacaccgcc gtcgctc 407
```

<210> 104

<211> 411

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Figure 7
consensus sequence

<220>

<221> modified_base

<222> (96)..(96)

<223> a, c, g, or t

<220>

<221> modified_base

<222> (106)..(106)

<223> a, c, g, or t

<220>

<221> modified_base

<222> (115)..(116)

<223> a, c, g, or t

<220>

<221> modified_base

<222> (118)..(119)

<223> a, c, g, or t

<220>

<221> modified_base

<222> (131)..(131)

<223> a, c, g, or t

<220>

<221> modified_base

<222> (158)..(158)

<223> a, c, g, or t

<400> 104

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ctctttcttg attttttggg tgggtggtgca tggccgttct tagttggtgg agtgatttgt 60
ctgcttaatt gcgataacga acgagacctc ggccctnctaa atagcncctg tccgnncnna 120
```

```

tttgccgggcc ngctggcttc ttagagggac tatcgggntc aagccgatgg aagtttgccg 180
caataacagg tctgtgatgc ccttagatgt tctgggccgc acgcgcgcta cactgacggg 240
gccagcgagt acataacctt ggccgagagg tctgggtaat cttgtgaaac cctgtcgtgc 300
tggggataga gcattgcaat tattgctctt caacgaggaa tgcctagtag gcgcgagtca 360
tcagctcgtg ttgattacgt ccctgccctt tgtacacacc gcccgtcgct a 411

```

```

<210> 105
<211> 19
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide primer

```

```

<400> 105
gtggtgctag catttgctg 19

```

```

<210> 106
<211> 17
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide primer

```

```

<400> 106
ccgctggctt cttaggg 17

```

```

<210> 107
<211> 18
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide primer

```

```

<400> 107
ggagccagcg agtctaac 18

```

```

<210> 108
<211> 19
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Synthetic

```

oligonucleotide primer

<400> 108
agggccagcg agtacatca 19

<210> 109
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 109
cggtttcaag ccgatggaag t 21

<210> 110
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 110
ctcaagccga tggaagtgcg 20

<210> 111
<211> 1500
<212> DNA
<213> Alicyclobacillus acidocaldarius

<400> 111
agagtttgat cctggctcag gacgaacgct ggcggcgtgc ctaatacatg caagtcgagc 60
gggtctcttc ggaggccagc ggcggacggg tgaggaacac gtgggtaatc tgcctttcag 120
gccggaataa cgcccggaaa cgggcgctaa agccggatac gcccgcgagg aggcattctc 180
ttgcggggga aggcccaatt gggtcgctga gagaggagcc cgcgcgcat tagctagttg 240
gcggggtaac ggcccaccaa ggcgacgatg cgtagccgac ctgagagggt gaccggccac 300
actgggactg agacacggcc cagactccta cgggaggcag cagtagggaa tcttccgcaa 360
tgggcgcaag cctgacggag caacgcgcgcg tgagcgaaga aggccttcgg gttgtaaagc 420
tctgttgctc ggggagagcg gcatggggga tggaaagccc cgtgcgagac ggtaccgagt 480
gaggaagccc cggctaacta cgtgccagca gccgcggtaa aacgtagggg gcgagcgttg 540
tccggaatca ctgggcgtaa aggggtgcgta ggcggtcgag caagtctgga gtgaaagtcc 600
atggctcaac catgggatgg ctttggaac tgcttgactt gagtgcgga gaggaagg 660
gaattccacg ttagcggtg aaatgcgtag agatgtggag gaataccagt ggcgaargcg 720
ccttgctgga cagtactga cgctgaggca cgaaagcgtg gggagcaaac aggattagat 780
accctggtag tccacgccgt aaacgatgag tgctaggtgt tgggggggaca caccctcagt 840
ccgaaggaaa mccaataagc actccgcctg gggagtacgg tcgcaagact gaaactcaaa 900
ggaattgacg ggggcccgcg caagcagtgg agcatgtggt ttaaactcgaa gcaacgcgaa 960
gaaccttacc agggcttgac atccctctga caccctcaga gatgaggggt cccttcgggg 1020
cagaggagac aggtggtgca tggttgtcgt cagctcgtgt cgtgagatgt tgggttcagt 1080

```

cccgcaacga gcgcaaccct tgacctgtgt taccagcgcg ttgaggcggg gactcacagg 1140
tgactgccgg cgtaagtcgg aggaaggcgg ggatgacgtc aaatcatcat gcccctgatg 1200
tcctgggcta cacacgtgct acaatgggcg gaacaaaggg aggcgaagcc gcgaggcgga 1260
gcgaaaccca aaaagccgct cgtagtccgg attgcaggct gcaactcgcc tgcatagaagc 1320
cggaattgct agtaatcgcg gatcagcatg ccgcgggtgaa tacgttcccg ggccttgtac 1380
acaccgcccc tcacaccacg agagtcggca acaccgaag tcggtgaggt aaccctgtg 1440
gggagccagc cgccgaaggt ggggtcgatg attggggtga agtcgtaaca aggtagccgt 1500

```

<210> 112

<211> 1520

<212> DNA

<213> Alicyclobacillus acidocaldarius

<220>

<221> modified_base

<222> (236)

<223> a, t, c or g

<220>

<221> modified_base

<222> (462)

<223> a, t, c or g

<400> 112

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gggtctcttc ggaggccagc ggcggacggg tgaggaaacac gtgggtaatc tgcctttcag 120
gccggaataa cgccccgaaa cgggcgctaa tgccggatac gcccgcgagg aggcattctc 180
ttgcggggga aggcccaatt gggccgctga gagaggagcc cgccggcgcat tagctngttg 240
gcggggtaac ggcccaccaa ggcgacgatg cgtagccgac ctgagagggt gaccggccac 300
actgggactg agacacggcc cagactccta cgggaggcag cagtagggaa tcttccgcaa 360
tgggcgcaag cctgacggag caacgcccg tgagcgaaga aggccttcgg gttgtaaagc 420
tctgttgctc ggggagagcg gcatggggga tggaaagccc cntgcgagac ggtaccgagt 480
gaggaagccc cggctaacta cgtgccagca gccgcggtaa aacgtagggg gcgagcgttg 540
tccggaatca ctgggcgtaa aggggtgcgt ggcggtcgag caagtctgga gtgaaagtcc 600
atggctcaac catgggatgg ctttggaaac tgcttgactt gagtgtgga gaggcaaggg 660
gaattccacg tgtagcgggtg aaatgcgtag agatgtggag gaataccagt ggcaaggcgg 720
ccttgctgga cagtactga cgtgaggca cgaaagcgtg gggagcaaac aggattagat 780
accctggtag tcacgccgt aaacgatgag tgctaggtgt tggggggaca caccctcagt 840
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tcctgggcta cacacgtgct acaatgggcg gaacaaaggg aggcgaagcc gcgaggcgga 1260
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cggaattgct agtaatcgcg gatcagcatg ccgcgggtgaa tacgttcccg ggccttgtac 1380
acaccgcccc tcacaccacg agagtcggca acaccgaag tcggtgaggt aaccctgtg 1440
gggagccagc cgccgaaggt ggggtcgatg attggggtga agtcgtaaca aggtagccgt 1500
accggaaggt gcggttgatg

```

<210> 113

<211> 1497

<212> DNA

<213> Alicyclobacillus cycloheptanicus

<400> 113

```

agagtttcat cctggctcag gacgaacgct ggccggcgtgc ctaatacatg caagtcgagc 60
ggacccttcg gggtcagcgg cggacgggtg agtaacacgt gggtaatctg cccaactgac 120
cggaataaac cctggaaacg ggtgctaagt ccgcataggg agcgagcagg catctgctcg 180
ctgggaaagg tgcaaatgca ccgcagatgg aggagcccgc ggcgcattag ctgggttggtg 240
gggtaacggc tcaccaaggc gacgatgcgt agccgacctg agaggggtgga cggccacact 300
gggactgaga cacggcccag actcctacgg gaggcagcag tagggaatct tccgcaatgg 360
gcgcaagcct gacggagcaa cgcgcgtga gcgaagaagg ccttcgggtt gtaaagctca 420
gtcactcggg aagagcggca aggggagtg aaagcccctt gagagacggg accgagagag 480
gaagccccgg ctaactacgt gccagcagcc gcgtaatac gtagggggca agcgttgctc 540
ggaatcactg ggcgtaaagc gtgcgtaggc ggttgctgtg gtccgggggtg aaagtcagg 600
gctcaaccct gggaatgcct tggaaactgc gtaacttgag tgctggagag gcaaggggaa 660
ttccgcgtgt agcgggtgaa tgcgtagata tgcggaggaa taccagtggc gaaggcgcct 720
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accgcccgtc acaccacgag agtcggcaac accggaagtc ggtggggtaa cccgtcaggg 1440
ggccagccgc cgaagggtgg gttgatgatt ggggtgaagt cgtaacaagg tagccgt 1497

```

<210> 114

<211> 1517

<212> DNA

<213> *Alicyclobacillus cycloheptanicus*

<400> 114

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ggacccttcg gggtcagcgg cggacgggtg agtaacacgt gggtaatctg cccaactgac 120
cggaataaac cctggaaacg ggtgctaagt ccgcataggg agcgagcagg catctgctcg 180
ctgggaaagg tgcaaatgca ccgcagatgg aggagcccgc ggcgcattag ctgggttggtg 240
gggtaacggc tcaccaaggc gacgatgcgt agccgacctg agaggggtgga cggccacact 300
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gtcactcggg aagagcggca aggggagtg aaagcccctt gagagacggg accgagagag 480
gaagccccgg ctaactacgt gccagcagcc gcgtaatac gtagggggca agcgttgctc 540
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ctgggctaca cacgtgctac aatgggcggg acaacgggaa gcgagaccgc gaggtggagc 1260
aaacccctga aagccgttcg tagttcggat tgcaggctgc aactcgctg catgaagccg 1320

```

```

gaattgctag taatcgcgga tcagcatgcc gcggtgaatc cgttcccggg ccttgtagac 1380
accgcccgtc acaccacgag agtcgggcaac acccgaagtc ggtggggtaa cccgtcaggg 1440
ggccagccgc cgaaggtggg gttgatgatt ggggtgaagt cgtaacaagg tagccgtatc 1500
ggaaggtgcg gttggat                                     1517

```

```

<210> 115
<211> 770
<212> DNA
<213> Alicyclobacillus acidoterrestris

```

```

<220>
<221> modified_base
<222> (549)..(549)
<223> a, c, g, or t

```

```

<220>
<221> modified_base
<222> (586)..(586)
<223> a, c, g, or t

```

```

<220>
<221> modified_base
<222> (595)..(595)
<223> a, c, g, or t

```

```

<220>
<221> modified_base
<222> (635)..(635)
<223> a, c, g, or t

```

```

<220>
<221> modified_base
<222> (640)..(640)
<223> a, c, g, or t

```

```

<220>
<221> modified_base
<222> (647)..(647)
<223> a, c, g, or t

```

```

<220>
<221> modified_base
<222> (661)..(661)
<223> a, c, g, or t

```

```

<220>
<221> modified_base
<222> (669)..(669)
<223> a, c, g, or t

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```

<220>
<221> modified_base
<222> (672)..(672)
<223> a, c, g, or t

```

<220>
 <221> modified_base
 <222> (696)..(696)
 <223> a, c, g, or t

<220>
 <221> modified_base
 <222> (699)..(699)
 <223> a, c, g, or t

<220>
 <221> modified_base
 <222> (742)..(742)
 <223> a, c, g, or t

<220>
 <221> modified_base
 <222> (751)..(751)
 <223> a, c, g, or t

<220>
 <221> modified_base
 <222> (756)..(756)
 <223> a, c, g, or t

<220>
 <221> modified_base
 <222> (763)..(763)
 <223> a, c, g, or t

<220>
 <221> modified_base
 <222> (770)..(770)
 <223> a, c, g, or t

<400> 115
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 ggtgctaata ccgataata cacgggtagg catctacttg tgttgaaaga tgcaactgca 180
 tcgctgagag aggagcccg cgcgcattag ctagttagtg aggtaacggc tcaccaaggc 240
 gacgatgcgt agccgacctg agaggggtgac cggccacact gggactgaga cacggcccag 300
 actcctacgg gaggcagcag tagggaatct tccgcaatgg gcgcaagcct gacggagcaa 360
 cgccgcgtga gcgaagaagg ccttcggggt gtaaagctct gttgctcggg gagagcgaca 420
 aggagagtgg aaagctcctt gtgagacggt accgagttag gaagccccgg ctaactacgt 480
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 cgtgcgtang cggttgtgta agtctgaact gaaagtccaa ggctcnacct tgggnatgct 600
 ttggaaactg catggacttg agtgctggag aggcnnagcn aattccnctg gttaccgggtg 660

naaatgcntgnt anatatgtgg aggaataacca gtggcnaang cgccttttgcg ggacagtggga 720
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<210> 116
 <211> 1514
 <212> DNA
 <213> Alicyclobacillus acidoterrestris

<400> 116
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 tggaataaca ctgcgaaacg ggtgctaatt ccggataata cacgggtagg catctacttg 180
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 gggactgaga cacggcccag actcctacgg gaggcagcag tagggaatct tccgcaatgg 360
 gcgcaagcct gacggagcaa cgcgcgctga gcgaagaagg ccttcggggt gttaaagctct 420
 gttgctcggg gagagcgaca aggagagtg aaagctcctt gtgagacgg accgagttag 480
 gaagccccgg ctaactacgt gccagcagcc gcggtataac gtagggggca agcgttgtcc 540
 ggaatcactg ggcgtaaagc gtgcgtaggg ggttgtgtaa gtctgaagt aaagtccaag 600
 gctcaacctt gggattgctt tggaaactgc atgacttgag tgctggagag gcaaggggaa 660
 ttccacgtgt agcgtgaaa tgctgagata tggaggagaa taccagtggc gaaggcgcct 720
 tgctggacag tgactgacgc tgaggcacga aagcgtgggg agcaaacagg attagatacc 780
 ctggtagtcc acgcgtaaa cgatgagtg taggtgttgg ggggacacac cccagtgcgc 840
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 attgacgggg gcccgacaaa gcagtggagc atgtggttta attcgaagca acgcgaagaa 960
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 tgggctacac acgtgctaca atgggcggta caacgggaag cgaagccgcg aggtggagca 1260
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 ccgcccgtca caccacgaga gtcggcaaca cccgaagtcg gtgaggtaac cgttatggag 1440
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<210> 117
 <211> 1492
 <212> DNA
 <213> Clostridium elmenteitii

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 gtaacgcgtg ggcaaccaac cttgatcagg gggacaacat tgggaaacca gtgctaatac 180
 cgcatagctc tatattatgg catcatgaga tagagaaaga tttatcggat caagacgggc 240
 ccgctctgga ttagctagtt ggtaaggtaa cggcttacca aggccttgat cagtaccga 300
 cctgagaggg tgaccggcca cactggaact gagacacggc ccagactcct acgggaggca 360
 gcagtgggga atattgcaca atgggggaaa ccctgatgca gcaacgccgc gtgagcgaag 420
 aaggccttcg ggtcgtaaa ctctgtccta tgggaagaag gagtgacgg accataggag 480
 gaagccccgg ctaactacgt gccagcagcc gcggtataac gtagggggca agcgttatcc 540


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tcctagtgtg gcggtgaaat gcgtagatat taggaggaac accagtggcg aaggcgactt 720
actggactgt aactgacgct gaggcacgaa agcgtgggag cgaacaggat tagataccct 780
ggtagtccac gccgtaaacg atgagtgtc ggtgttggg gtcaaacctc agtgccggag 840
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gacgggggac ccgcacaagc agcggagcat gtggtttaat tcgaagcaac gcgaagaacc 960
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ttgctagtaa tcgcgaatca gcatgtcgcg gtgaatgcgt tcccggtct tgtacacacc 1380
gcccgtcaca ccacggaagt cggaagcacc cgaagcccg taccgaacct tcgggacgga 1440
acggtcgaag gtgaagccga taactggggt gaagtcgtaa caaggtatcc gt 1492

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<210> 118

<211> 1548

<212> DNA

<213> *Geobacillus subterraneus*

<400> 118

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acctgcccgc aagaccggga taactccggg aaaccggagc taataccgga taacaccgaa 180
gaccgcatgg tcttcgggtg aaaggcggcc tttggctgtc acttgcggtt gggcccgcgg 240
cgatttagct agttggtgag gtaacggctc accaaggcga cgatgcgtag ccggcctgag 300
aggggtgacc gccacactgg gactgagaca cggcccagac tcctacggga ggagcagta 360
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ttcggtgctg aaagctctgt tgtgagggac gaaggagcgc cgtttgaaca aggcggcgcg 480
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caggagagga gagcggaatt ccacgtgtag cggtgaaatg cgtagagatg tggaggaaca 720
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gctgcaaac cgcgaggggg agcgaatccc aaaaagccgc tctcagttcg gattgcaggc 1320
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<210> 119

<211> 1496

<212> DNA

<213> *Sulfobacillus disulfidooxidans*

<400> 119

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gtgtgggaaa gatgtacgg catcgccagt ggaggagccc gcggcgcat t agctggttg 240
cggggtaacg gaccaccaag gcgacgatgc gtaccgacc tgagaggggtg aacggccaca 300
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caccgcccgt cacaccacga gactcgacaa caccggaagt cgggtgggta accgtaagg 1440
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<210> 120

<211> 1428

<212> DNA

<213> *Bacillus thermoleovorans*

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<223> a, t, c or g

<400> 120

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ctgcccgcaa gaccgggata actccgggaa accggagcta ataccggata acaccgaaga 180
ccgcatggtc tttggttgaa aggcggcttt ggctgtcact tgcggatggg cccgcggcgc 240
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gggtcgtaaa gctctgttgt gagggacgaa ggagcgccgt tcgaagaggg cggcgcggtg 480
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gggcgagcgt tgtccggaat tattggcgt aaagcgcgcg caggcggttc cttaagtctg 600
atgtgaaagc ccacggctca accgtggagg gtcattggaa actgggggac ttgagtgcag 660
gagaggagag cggaattcca cgtgtagcgg tgaaatgcgt agagatgtgg aggaacacca 720
gtggcgagg cggtctctctg gcctgcaact gacgtgagg cgcgaaagct ggggagcaaa 780
caggattaga taccctggta gtccacgccg taaacgatga gtgctaagt ttagaggggt 840
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gaagcaacgc gaagaacctt accaggtctt gacatccct gacaacccaa gagattggg 1020
gttccttcgg gggacagggt gacaggtggt gcatggttgt cgtcagctcg tgtcgtgaga 1080

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atgcccctta tgacctgggc tacacacgtg ctacaatggg cggtacaaag ggctgcgaac 1260
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cctgcatgaa gccggaatcg ctagtaatcg cggatcagca tgccgcggtg aatacgttcc 1380
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<210> 121

<211> 1528

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Figure 8
consensus sequence

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<222> (132)..(132)

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<222> (164)..(164)

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<221> modified_base

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<223> a, c, g, t or not present

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<223> a, c, g, t or not present

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<223> a, c, g, t or not present

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<223> a, c, g, t or not present

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<223> a, c, g, t or not present

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<222> (1438)..(1440)
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<220>
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<222> (1501)..(1528)

<223> a, c, g, t or not present

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accggaataa cncnngaaa cgggtgctaa tgccggatan nncncgagna ggcattctnct	180
tgngngaaaa ggtgcaantg natcgctgan ngaggagccc gcggcgcatc agctagttgg	240
tgnggtaacg gctcaccaag gcgacgatgc gtagccgacc tgagaggggtg accggccaca	300
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ctgttgctcg ggaagagcgg cangngngt ggaaagcncc ntgngagacg gtaccgagng	480
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ccggaatcac tgggcgtaaa gcgtgcgtag gcggttngt aagtctgnng tgaaagtcca	600
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Figure 8
consensus sequence

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majority sequence

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